

DOUBLE-STRANDED CONFORMATIONAL POLYMORPHISM ANALYSIS

ABSTRACT OF THE DISCLOSURE

Double-stranded conformational polymorphism analysis is performed by combining a probe comprising a cross-linking agent and optionally a label with a sample having a target sequence, which may be complementary or have one or a few mismatches with respect to the probe sequence. After sufficient time for hybridization under mild or lesser stringency conditions, hybridized pairs are irradiated to induce cross-link formation by the cross-linking agent. The sample is then analyzed by denaturing gel electrophoresis where the rate of migration depends upon the degree of complementarity between the probe and the target. For corroboration, in a second experiment, the probe may be combined with the sample under high stringency conditions, where it is found that the formation of cross-linked probe/target is substantially lower for pairs having mismatches than for fully matched pairs. After cross-linking, the sample may be separated by gel electrophoresis, and the amount of cross-linked nucleic acid determined.